Microbiol Resour Announc. 2021 Sep 16;10(37):e00751-21. doi: 10.1128/MRA.00751-21

Draft Genome Sequences of Fungi Isolated from the International Space Station during the Microbial Tracking-2 Experiment

Anna C Simpson [a], Camilla Urbaniak [a], John R Bateh [a], Nitin K Singh [a], Jason M Wood [a,*], Marilyne Debieu [b], Niamh B O'Hara [b,c], Jos Houbraken [d], Christopher E Mason [e,f], Kasthuri Venkateswaran [a,✉]

Editor: Vincent Bruno[g]

Author information Article notes Copyright and License information
PMCID: PMC8444978 PMID: 34528817

ABSTRACT

As part of the Microbial Tracking-2 study, 94 fungal strains were isolated from surfaces on the International Space Station, and whole-genome sequences were assembled. Characterization of these draft genomes will allow evaluation of microgravity adaption, risks to human health and spacecraft functioning, and biotechnological applications of fungi.

ANNOUNCEMENT

Fungi are potential sources of nutrients and bioactive compounds during long-term spaceflight but also could affect astronaut health through both opportunistic infections and system biofouling (1, 2). As part of a study characterizing fungal responses to the space environment, we report the draft genomes of 94 fungal strains that were isolated from the International Space Station (ISS), representing 10 ascomycetous and 1 basidiomycetous species.

Aspergillus species are environmental fungi and opportunistic pathogens (3). *Aspergillus unguis* is a member of the ISS microbiome (4) and produces industrially important compounds (5). *Aureobasidium pullulans* is a black fungus that was previously isolated from the ISS water filtration system (6) and Mars mission spacecraft-associated surfaces (7).

Cladosporium species are dominant fungal contaminants in indoor air (8, 9). *Cladosporium sphaerospermum* and *Cladosporium cladosporioides* were detected multiple time on the ISS, and their properties in microgravity were studied (10, 11).

Fusarium veterinarium is a recently described species within the *Fusarium oxysporum* complex, the species of which are ubiquitous in soil, are known human/plant pathogens (12), and were isolated both from surfaces and from infected *Zinnia hybrida* plants aboard the ISS (13, 14). *Fusarium annulatum*, which has been isolated from plant and human tissues on Earth, has not been reported previously in space (15).

Penicillium species produce important bioactive compounds and can contaminate food and cause secondary infections (16). Previously detected on the ISS or Mir (2, 11) are *Penicillium citrinum*, a common soil and indoor species (17), *Penicillium rubens*, from which penicillin was isolated (18), and *Penicillium corylophilum*, which is commonly found in damp buildings (19). *Penicillium palitans*, which has been reported in cheese (20) and also in a wide range of habitats, including Antarctica (21), has not been reported previously in space.

Rhodotorula mucilaginosa is a ubiquitous environmental (22) and human commensal yeast and opportunistic pathogen (23) that is found in aquatic and built environments, including bathrooms and dishwashers (24, 25). It is the most commonly isolated yeast on the ISS (26–28).

Sample collection and fungal isolation steps were described elsewhere (26). For five flight missions, eight surfaces aboard the ISS were sampled with moistened polyester wipes (Table 1). Upon return to Earth, the wipes were agitated in sterile phosphate-buffered saline, which was concentrated using an InnovaPrep CP150 concentrating pipette, and suitable aliquots were spread onto nutrient media (Table 1). Fungal isolates were restreaked on potato-dextrose agar (PDA), and genomic DNA was extracted using the ZymoBIOMICS MagBead DNA kit according to the manufacturer's instructions. Whole-genome shotgun sequencing libraries were prepared with an Illumina Nextera DNA Flex library preparation kit (29) and were sequenced on the NovaSeq 6000 paired-end 2 × 150-bp platform with a S4 flow cell. After quality filtering and trimming with FastQC v0.11.7 (30) and fastp v0.20.0 (31), genomes were assembled using SPAdes v3.11.1 (32). Assembly quality was assessed with QUAST v5.0.2 (33). Fastp included screening for 512 adapters; otherwise, default settings were used for all steps.

TABLE 1.

Sampling locations, genetic loci used for taxonomic analysis, and WGS assembly quality for fungal species isolated from the ISS during the Microbial Tracking-2 mission

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F6_8S_P_2A	*Aspergillus unguis*	*benA*, *CaM*	JAGUQD000000000	SRR14342084	BA, 37°C	F6
F6_8S_P_4A	*Aspergillus unguis*	*benA*, *CaM*	JAGUQC000000000	SRR14342083	BA, 37°C	F6
F7_6S_YPD	*Aureobasidium pullulans*	ITS	JAGUPW000000000	SRR14342072	YPD, 25°C	F7
F7_5S_YPD	*Aureobasidium pullulans*	ITS	JAGUPX000000000	SRR14342073	YPD, 25°C	F7
F7_2S_YPD	*Aureobasidium pullulans*	ITS	JAGUPY000000000	SRR14342074	YPD, 25°C	F7
F7_1S_YPD	*Aureobasidium pullulans*	ITS	JAGUQA000000000	SRR14342076	YPD, 25°C	F7
F7_2A_YPD	*Aureobasidium pullulans*	ITS	JAGUPZ000000000	SRR14342075	YPD, 25°C	F7
F7_1A_YPD	*Aureobasidium pullulans*	ITS	JAGUQB000000000	SRR14342077	YPD, 25°C	F7
F6_1S_B_1B	*Aureobasidium pullulans*	ITS	JAGUQJ000000000	SRR14342071	R2A, 25°C	F6
F6_1S_P_3A	*Aureobasidium pullulans*	ITS	JAGUQI000000000	SRR14342125	BA, 37°C	F6
F6_4S_B_1	*Aureobasidium pullulans*	ITS	JAGUQE000000000	SRR14342118	R2A, 25°C	F6
F6_3S_1A_F	*Aureobasidium pullulans*	ITS	JAGUQH000000000	SRR14342124	PDA, 25°C	F6

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F6_3S_1B_F	*Aureobasidium pullulans*	ITS	JAGUQG000000000	SRR14342123	PDA, 25°C	F6
F6_3S_1C_F	*Aureobasidium pullulans*	ITS	JAGUQF000000000	SRR14342122	PDA, 25°C	F6
F8_5S_2F	*Cladosporium cladosporioides*	*TEF*	JAGUPV000000000	SRR14342051	PDA, 25°C	F8
F8_5S_3F	*Cladosporium cladosporioides*	*TEF*	JAGUPU000000000	SRR14342048	PDA, 25°C	F8
F8_5S_4F	*Cladosporium cladosporioides*	*TEF*	JAGUPT000000000	SRR14342047	PDA, 25°C	F8
F4_7S_F1_F	*Cladosporium sphaerospermum*	*TEF*	JAHARS000000000	SRR14342126	PDA, 25°C	F4
F8_4S_2B	*Fusarium annulatum*	*TEF*, *RPB2*	JAHAPR000000000	SRR14342059	R2A, 25°C	F8
F8_4S_3B	*Fusarium annulatum*	TEF, *RPB2*	JAHAPP000000000	SRR14342057	R2A, 25°C	F8
F8_4S_4P	*Fusarium annulatum*	*TEF*, *RPB2*	JAHAPN000000000	SRR14342055	BA, 37°C	F8
F8_4S_5P	*Fusarium annulatum*	*TEF*, *RPB2*	JAHAPL000000000	SRR14342053	BA, 37°C	F8
F8_4S_1F	*Fusarium annulatum*	*TEF*, *RPB2*	JAHAPT000000000	SRR14342062	PDA, 25°C	F8
F5_8S_1A_F	*Fusarium veterinarium*	*TEF*	JAHARR000000000	SRR14342093	PDA, 25°C	F5
F5_8S_1B_F	*Fusarium veterinarium*	*TEF*	JAHARQ000000000	SRR14342082	PDA, 25°C	F5
F4_1A_F1_F	*Penicillium citrinum*	*benA*, *CaM*	JAHART000000000	SRR14342127	PDA, 25°C	F4
F5_1S_1A_F	*Penicillium corylophilum*	*benA*, *CaM*	JAGUQL000000000	SRR14342115	PDA, 25°C	F5

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F5_1S_1B_F	*Penicillium corylophilum*	*benA*, *CaM*	JAGUQK000000000	SRR14342104	PDA, 25°C	F5
F6_4S_1A_F	*Penicillium palitans*	*benA*, *CaM*	JAHARM000000000	SRR14342121	PDA, 25°C	F6
F6_4S_1B_F	*Penicillium palitans*	*benA*, *CaM*	JAHARL000000000	SRR14342120	PDA, 25°C	F6
F6_4S_1C_F	*Penicillium palitans*	*benA*, *CaM*	JAHARK000000000	SRR14342119	PDA, 25°C	F6
F6_6S_1_F	*Penicillium palitans*	*benA*, *CaM*	JAHARA000000000	SRR14342107	PDA, 25°C	F6
F6_7S_1A_F	*Penicillium palitans*	*benA*, *CaM*	JAHAQR000000000	SRR14342097	PDA, 25°C	F6
F6_7S_1C_F	*Penicillium palitans*	*benA*, *CaM*	JAHAQQ000000000	SRR14342096	PDA, 25°C	F6
F6_8S_1A_F	*Penicillium palitans*	*benA*, *CaM*	JAHAQI000000000	SRR14342087	PDA, 25°C	F6
F6_8S_1C_F	*Penicillium palitans*	*benA*, *CaM*	JAHAQH000000000	SRR14342086	PDA, 25°C	F6
F8_6S-1F	*Penicillium palitans*	*benA*, *CaM*	JAHAOZ000000000	SRR14342036	PDA, 25°C	F8
F8_6S_2F	*Penicillium palitans*	*benA*, *CaM*	JAHAPD000000000	SRR14342041	PDA, 25°C	F8
F8_6S-3F	*Penicillium palitans*	*benA*, *CaM*	JAHAOY000000000	SRR14342035	PDA, 25°C	F8
F8_6S-4F	*Penicillium palitans*	*benA*, *CaM*	JAHAOX000000000	SRR14342034	PDA, 25°C	F8
F8_6S_5F	*Penicillium palitans*	*benA*, *CaM*	JAHAPC000000000	SRR14342040	PDA, 25°C	F8
F8_6S_6F	*Penicillium rubens*	*benA*, *CaM*	JAHAPB000000000	SRR14342039	PDA, 25°C	F8

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F8_6S_7F	*Penicillium rubens*	*benA*, *CaM*	JAHAPA000000000	SRR14342037	PDA, 25°C	F8
F6_4S_B_2B	*Rhodotorula mucilaginosa*	ITS	JAHARI000000000	SRR14342116	R2A, 25°C	F6
F6_8S_B_1B	*Rhodotorula mucilaginosa*	ITS	JAHAQG000000000	SRR14342085	R2A, 25°C	F6
F6_8S_P_5A	*Rhodotorula mucilaginosa*	ITS	JAHAQF000000000	SRR14342081	BA, 37°C	F6
F6_8S_P_5B	*Rhodotorula mucilaginosa*	ITS	JAHAQE000000000	SRR14342080	BA, 37°C	F6
F6_8S_P_6A	*Rhodotorula mucilaginosa*	ITS	JAHAQD000000000	SRR14342079	BA, 37°C	F6
F6_8S_P_6B	*Rhodotorula mucilaginosa*	ITS	JAHAQC000000000	SRR14342078	BA, 37°C	F6
F8_5S_4P	*Rhodotorula mucilaginosa*	ITS	JAHAPI000000000	SRR14342046	BA, 37°C	F8
F8_5S_5P	*Rhodotorula mucilaginosa*	ITS	JAHAPH000000000	SRR14342045	BA, 37°C	F8
F8_5S_6P	*Rhodotorula mucilaginosa*	ITS	JAHAPG000000000	SRR14342044	BA, 37°C	F8
F6_1S_P_1A	*Rhodotorula mucilaginosa*	ITS	JAHARP000000000	SRR14342060	BA, 37°C	F6
F6_1S_P_1B	*Rhodotorula mucilaginosa*	ITS	JAHARO000000000	SRR14342049	BA, 37°C	F6
F6_1S_P_1C	*Rhodotorula mucilaginosa*	ITS	JAHARN000000000	SRR14342038	BA, 37°C	F6
F6_4S_B_2A	*Rhodotorula mucilaginosa*	ITS	JAHARJ000000000	SRR14342117	R2A, 25°C	F6
F6_4S_B_2C	*Rhodotorula mucilaginosa*	ITS	JAHARH000000000	SRR14342114	R2A, 25°C	F6

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F6_4S_P_3B	*Rhodotorula mucilaginosa*	ITS	JAHARG000000000	SRR14342113	BA, 37°C	F6
F6_4S_P_3C	*Rhodotorula mucilaginosa*	ITS	JAHARF000000000	SRR14342112	BA, 37°C	F6
F6_4S_P_4A	*Rhodotorula mucilaginosa*	ITS	JAHARE000000000	SRR14342111	BA, 37°C	F6
F6_4S_P_4B	*Rhodotorula mucilaginosa*	ITS	JAHARD000000000	SRR14342110	BA, 37°C	F6
F6_4S_P_5A	*Rhodotorula mucilaginosa*	ITS	JAHARC000000000	SRR14342109	BA, 37°C	F6
F6_4S_P_5B	*Rhodotorula mucilaginosa*	ITS	JAHARB000000000	SRR14342108	BA, 37°C	F6
F6_6S_B_1A	*Rhodotorula mucilaginosa*	ITS	JAHAQZ000000000	SRR14342106	R2A, 25°C	F6
F6_6S_B_1B	*Rhodotorula mucilaginosa*	ITS	JAHAQY000000000	SRR14342105	R2A, 25°C	F6
F6_6S_B_1C	*Rhodotorula mucilaginosa*	ITS	JAHAQX000000000	SRR14342103	R2A, 25°C	F6
F6_6S_P_1A	*Rhodotorula mucilaginosa*	ITS	JAHAQW000000000	SRR14342102	BA, 37°C	F6
F6_6S_P_1B	*Rhodotorula mucilaginosa*	ITS	JAHAQV000000000	SRR14342101	BA, 37°C	F6
F6_6S_P_1C	*Rhodotorula mucilaginosa*	ITS	JAHAQU000000000	SRR14342100	BA, 37°C	F6
F6_6S_P_2A	*Rhodotorula mucilaginosa*	ITS	JAHAQT000000000	SRR14342099	BA, 37°C	F6
F6_6S_P_2B	*Rhodotorula mucilaginosa*	ITS	JAHAQS000000000	SRR14342098	BA, 37°C	F6
F6_7S_B_2A	*Rhodotorula mucilaginosa*	ITS	JAHAQP000000000	SRR14342095	R2A, 25°C	F6

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F6_7S_B_2B	*Rhodotorula mucilaginosa*	ITS	JAHAQO000000000	SRR14342094	R2A, 25°C	F6
F6_7S_B_2C	*Rhodotorula mucilaginosa*	ITS	JAHAQN000000000	SRR14342092	R2A, 25°C	F6
F6_7S_P_6B	*Rhodotorula mucilaginosa*	ITS	JAHAQM000000000	SRR14342091	BA, 37°C	F6
F6_7S_P_7A	*Rhodotorula mucilaginosa*	ITS	JAHAQL000000000	SRR14342090	BA, 37°C	F6
F6_7S_P_7B	*Rhodotorula mucilaginosa*	ITS	JAHAQK000000000	SRR14342089	BA, 37°C	F6
F6_7S_P_7C	*Rhodotorula mucilaginosa*	ITS	JAHAQJ000000000	SRR14342088	BA, 37°C	F6
F8_1S_2B	*Rhodotorula mucilaginosa*	ITS	JAHAQB000000000	SRR14342070	R2A, 25°C	F8
F8_1S_3B	*Rhodotorula mucilaginosa*	ITS	JAHAQA000000000	SRR14342069	R2A, 25°C	F8
F8_3S_1B	*Rhodotorula mucilaginosa*	ITS	JAHAPZ000000000	SRR14342068	R2A, 25°C	F8
F8_3S_2B	*Rhodotorula mucilaginosa*	ITS	JAHAPX000000000	SRR14342066	R2A, 25°C	F8
F8_3S_3B	*Rhodotorula mucilaginosa*	ITS	JAHAPV000000000	SRR14342064	R2A, 25°C	F8
F8_4S_4B	*Rhodotorula mucilaginosa*	ITS	JAHAPO000000000	SRR14342056	R2A, 25°C	F8
F8_4S_5B	*Rhodotorula mucilaginosa*	ITS	JAHAPM000000000	SRR14342054	R2A, 25°C	F8
F8_5S_2B	*Rhodotorula mucilaginosa*	ITS	JAHAPK000000000	SRR14342052	R2A, 25°C	F8
F8_5S_3B	*Rhodotorula mucilaginosa*	ITS	JAHAPJ000000000	SRR14342050	R2A, 25°C	F8

Sample name	Fungal species	Loci used for identification[a]	WGS accession no.	SRA accession no.	Medium and temperature[b]	Flig no
F8_6S_1B	*Rhodotorula mucilaginosa*	ITS	JAHAPF000000000	SRR14342043	R2A, 25°C	F8
F8_6S_2B	*Rhodotorula mucilaginosa*	ITS	JAHAPE000000000	SRR14342042	R2A, 25°C	F8
F8_3S_1P	*Rhodotorula mucilaginosa*	ITS	JAHAPY000000000	SRR14342067	BA, 37°C	F8
F8_3S_2P	*Rhodotorula mucilaginosa*	ITS	JAHAPW000000000	SRR14342065	BA, 37°C	F8
F8_3S_3P	*Rhodotorula mucilaginosa*	ITS	JAHAPU000000000	SRR14342063	BA, 37°C	F8
F8_4S_1P	*Rhodotorula mucilaginosa*	ITS	JAHAPS000000000	SRR14342061	BA, 37°C	F8
F8_4S_2P	*Rhodotorula mucilaginosa*	ITS	JAHAPQ000000000	SRR14342058	BA, 37°C	F8

Open in a new tab

[a]*benA*, β-tubulin; *CaM*, calmodulin; *RPB2*, DNA-directed RNA polymerase II subunit; *TEF*, translation elongation factor 1.
[b]BA, blood agar; R2A, Reasoner's 2A agar; YPD, yeast extract-peptone-dextrose.
[c]ARED, advanced resistive exercise device; WHC, waste and hygiene compartment; PMM, permanent multipurpose module.
[d]Reference genome was not available; average sequencing depth was calculated from *k*-mer coverage.

Genus-level identification was made via BLAST searches against the UNITE nuclear ribosomal internal transcribed spacer (ITS) database (34). Species identification was performed using specific loci suitable for species recognition (Table 1) (35). Homology searches were performed with extracted sequences against the NCBI nucleotide database and in-house Westerdijk Fungal Biodiversity Institute databases containing reference sequences; in case of doubt, identification was confirmed by constructing phylograms.

Data availability.

The whole-genome sequences (WGSs) and raw data have been deposited in GenBank under BioProject accession number PRJNA723004. This project has also been deposited in the NASA GeneLab system (36) under project number GLDS-400. The version described in this paper is the first version.

ACKNOWLEDGMENTS

Part of the research described was carried out at the Jet Propulsion Laboratory (JPL) of the California Institute of Technology under a contract with NASA. This research was funded by a 2014 Space Biology NNH14ZTT002N award (grant 80NSSC18K0113) to Crystal Jaing and K.V., which also partially funded postdoctoral fellowships for C.U. and J.M.W. Additionally, A.C.S. was supported by grant 80NM0018D0004, funded to K.V.

We thank astronauts Colonel Jack Fischer, Colonel Mark Vande Hei, Norishige Kanai, and Alexander Gerst for collecting samples aboard the ISS, the implementation team (Fathi Karouia) at NASA Ames Research Center for coordinating this effort, and Crystal Jaing (Lawrence Livermore National Laboratory), principal investigator of the team. We thank Ryan Kemp (Zymo Corp.) for extracting the DNA and Dan Butler (Weill Cornell Medicine) for generating the shotgun sequencing. The JPL supercomputing facility staff is acknowledged, notably, Narendra J. Patel (Jimmy) and Edward Villanueva, for their continuous support in providing the best possible infrastructure for BIG-DATA analysis.

Contributor Information

Kasthuri Venkateswaran, Email: kjvenkat@jpl.nasa.gov.

Vincent Bruno, University of Maryland School of Medicine.

REFERENCES

1. Romsdahl J, Blachowicz A, Chiang AJ, Chiang YM, Masonjones S, Yaegashi J, Countryman S, Karouia F, Kalkum M, Stajich JE, Venkateswaran K, Wang CCC. 2019. International Space Station conditions alter genomics, proteomics, and metabolomics in *Aspergillus nidulans*. Appl Microbiol Biotechnol 103:1363–1377. doi: 10.1007/s00253-018-9525-0. [DOI] [PMC free article] [PubMed] [Google Scholar]

2. Klintworth R, Reher H, Viktorov A, Bohle D. 1999. Biological induced corrosion of materials II: new test methods and experiences from MIR station. Acta Astronaut 44:569–578. doi: 10.1016/

s0094-5765(99)00069-7. [DOI] [PubMed] [Google Scholar]

3. Hogan LH, Klein BS, Levitz SM. 1996. Virulence factors of medically important fungi. Clin Microbiol Rev 9:469–488. doi: 10.1128/CMR.9.4.469. [DOI] [PMC free article] [PubMed] [Google Scholar]

4. Mora M, Wink L, Kogler I, Mahnert A, Rettberg P, Schwendner P, Demets R, Cockell C, Alekhova T, Klingl A, Krause R, Zolotariof A, Alexandrova A, Moissl-Eichinger C. 2019. Space Station conditions are selective but do not alter microbial characteristics relevant to human health. Nat Commun 10:3990. doi: 10.1038/s41467-019-11682-z. [DOI] [PMC free article] [PubMed] [Google Scholar]

5. Molina G, Contesini F, De Melo R, Sato H, Pastore G. 2016. β-Glucosidase from *Aspergillus*, p 155–169. *In* Gupta V (ed), New and future developments in microbial biotechnology and bioengineering. Elsevier, Amsterdam, Netherlands. [Google Scholar]

6. La Duc MT, Sumner R, Pierson D, Venkat P, Venkateswaran K. 2004. Evidence of pathogenic microbes in the International Space Station drinking water: reason for concern? Habitation (Elmsford) 10:39–48. doi: 10.3727/154296604774808883. [DOI] [PubMed] [Google Scholar]

7. La Duc MT, Nicholson W, Kern R, Venkateswaran K. 2003. Microbial characterization of the Mars Odyssey spacecraft and its encapsulation facility. Environ Microbiol 5:977–985. doi: 10.1046/j.1462-2920.2003.00496.x. [DOI] [PubMed] [Google Scholar]

8. Bensch K, Groenewald J, Meijer M, Dijksterhuis J, Jurjević Ž, Andersen B, Houbraken J, Crous PW, Samson R. 2018. *Cladosporium* species in indoor environments. Stud Mycol 89:177–301. doi: 10.1016/j.simyco.2018.03.002. [DOI] [PMC free article] [PubMed] [Google Scholar]

9. Aihara M, Tanaka T, Takatori K. 2001. *Cladosporium* as the main fungal contaminant of locations in dwelling environments. Biocontrol Sci 6:49–52. doi: 10.4265/bio.6.49. [DOI] [Google Scholar]

10. Singh NK, Blachowicz A, Romsdahl J, Wang C, Torok T, Venkateswaran K. 2017. Draft genome sequences of several fungal strains selected for exposure to microgravity at the International Space Station. Genome Announc 5:e01602-16. doi: 10.1128/genomeA.01602-16. [DOI] [PMC free article] [PubMed] [Google Scholar]

11. Satoh K, Yamazaki T, Nakayama T, Umeda Y, Alshahni MM, Makimura M, Makimura K. 2016. Characterization of fungi isolated from the equipment used in the International Space Station or Space Shuttle. Microbiol Immunol 60:295–302. doi: 10.1111/1348-0421.12375. [DOI] [PubMed] [Google Scholar]

12. Laurence MH, Summerell BA, Burgess LW, Liew EC. 2014. Genealogical concordance phylogenetic species recognition in the *Fusarium oxysporum* species complex. Fungal Biol 118:374–384. doi: 10.1016/j.funbio.2014.02.002. [DOI] [PubMed] [Google Scholar]

13. Urbaniak C, van Dam P, Zaborin A, Zaborina O, Gilbert JA, Torok T, Wang CCC, Venkateswaran K. 2019. Genomic characterization and virulence potential of two *Fusarium oxysporum* isolates cultured from the International Space Station. mSystems 4:e00345-18. doi: 10.1128/mSystems.00345-18. [DOI] [PMC free article] [PubMed] [Google Scholar]

14. Schuerger AC, Amaradasa BS, Dufault NS, Hummerick ME, Richards JT, Khodadad CL, Smith TM, Massa GD. 2021. *Fusarium oxysporum* as an opportunistic fungal pathogen on *Zinnia hybrida* plants grown on board the International Space Station. Astrobiology doi: 10.1089/ast.2020.2399. [DOI] [PubMed] [Google Scholar]

15. Khazaal FAK, Ameen MKM, Ali HA. 2019. Pathogenic fungi accompanied with sudden decline syndrome (wilting disease) of date palm tree (*Phoenix dactylifera* L.). Basrah J Sci 37:376–397. [Google Scholar]

16. Visagie CM, Houbraken J, Frisvad JC, Hong SB, Klaassen CH, Perrone G, Seifert KA, Varga J, Yaguchi T, Samson RA. 2014. Identification and nomenclature of the genus *Penicillium*. Stud Mycol 78:343–371. doi: 10.1016/j.simyco.2014.09.001. [DOI] [PMC free article] [PubMed] [Google Scholar]

17. Houbraken J, Frisvad JC, Samson R. 2011. Taxonomy of *Penicillium* section *Citrina*. Stud Mycol 70:53–138. doi: 10.3114/sim.2011.70.02. [DOI] [PMC free article] [PubMed] [Google Scholar]

18. Boruta T. 2018. Uncovering the repertoire of fungal secondary metabolites: from Fleming's laboratory to the International Space Station. Bioengineered 9:12–16. doi: 10.1080/21655979.2017.1341022. [DOI] [PMC free article] [PubMed] [Google Scholar]

19. McMullin DR, Nsiama TK, Miller JD. 2014. Secondary metabolites from *Penicillium corylophilum* isolated from damp buildings. Mycologia 106:621–628. doi: 10.3852/13-265. [DOI] [PubMed] [Google Scholar]

20. Kure C, Abeln E, Holst-Jensen A, Skaar I. 2002. Differentiation of *Penicillium commune* and *Penicillium palitans* isolates from cheese and indoor environments of cheese factories using M13 fingerprinting. Food Microbiol 19:151–157. doi: 10.1006/fmic.2001.0473. [DOI] [Google Scholar]

21. de Menezes GCA, Porto BA, Amorim SS, Zani CL, de Almeida Alves TM, Junior PAS, Murta SMF, Simões JC, Cota BB, Rosa CA, Rosa LH. 2020. Fungi in glacial ice of Antarctica: diversity, distribution and bioprospecting of bioactive compounds. Extremophiles 24:367–376. doi: 10.1007/s00792-020-01161-5. [DOI] [PubMed] [Google Scholar]

22. Libkind D, Brizzio S, van Broock M. 2004. *Rhodotorula mucilaginosa*, a carotenoid producing yeast strain from a Patagonian high-altitude lake. Folia Microbiol (Praha) 49:19–25. doi: 10.1007/BF02931640. [DOI] [PubMed] [Google Scholar]

23. Wirth F, Goldani LZ. 2012. Epidemiology of *Rhodotorula*: an emerging pathogen. Interdiscip Perspect Infect Dis 2012:465717. doi: 10.1155/2012/465717. [DOI] [PMC free article] [PubMed] [Google Scholar]

24. Gümral R, Özhak-Baysan B, Tümgör A, Saraçlı MA, Yıldıran ŞT, Ilkit M, Zupančič J, Novak-Babič M, Gunde-Cimerman N, Zalar P, de Hoog GS. 2016. Dishwashers provide a selective extreme environment for human-opportunistic yeast-like fungi. Fungal Diversity 76:1–9. doi: 10.1007/s13225-015-0327-8. [DOI] [Google Scholar]

25. Rai S, Singh DK, Kumar A. 2021. Microbial, environmental and anthropogenic factors influencing the indoor microbiome of the built environment. J Basic Microbiol 61:267–292. doi: 10.1002/jobm.202000575. [DOI] [PubMed] [Google Scholar]

26. Checinska Sielaff A, Urbaniak C, Mohan GBM, Stepanov VG, Tran Q, Wood JM, Minich J, McDonald D, Mayer T, Knight R, Karouia F, Fox GE, Venkateswaran K. 2019. Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome 7:50. doi: 10.1186/s40168-019-0666-x. [DOI] [PMC free article] [PubMed] [Google Scholar]

27. Daudu R, Parker CW, Singh NK, Wood JM, Debieu M, O'Hara NB, Mason CE, Venkateswaran K. 2020. Draft genome sequences of *Rhodotorula mucilaginosa* strains isolated from the International Space Station. Microbiol Resour Announc 9:e00570-20. doi: 10.1128/MRA.00570-20. [DOI] [PMC free article] [PubMed] [Google Scholar]

28. Sugita T, Yamazaki T, Cho O, Furukawa S, Mukai C. 2021. The skin mycobiome of an astronaut during a 1-year stay on the International Space Station. Med Mycol 59:106–109. doi: 10.1093/mmy/myaa067. [DOI] [PubMed] [Google Scholar]

29. Be NA, Avila-Herrera A, Allen JE, Singh N, Checinska Sielaff A, Jaing C, Venkateswaran K. 2017. Whole metagenome profiles of particulates collected from the International Space Station. Microbiome 5:81. doi: 10.1186/s40168-017-0292-4. [DOI] [PMC free article] [PubMed] [Google Scholar]

30. Andrews S. 2011. FastQC: a quality control tool for high throughput sequence data. Babraham Institute, Cambridge, UK. https://www.bioinformatics.babraham.ac.uk/projects/fastqc. [Google Scholar]

31. Chen S, Zhou Y, Chen Y, Gu J. 2018. fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34:i884–i890. doi: 10.1093/bioinformatics/bty560. [DOI] [PMC free article] [PubMed] [Google Scholar]

32. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. doi: 10.1089/cmb.2012.0021. [DOI] [PMC free article] [PubMed] [Google Scholar]

33. Gurevich A, Saveliev V, Vyahhi N, Tesler G. 2013. QUAST: quality assessment tool for genome assemblies. Bioinformatics 29:1072–1075. doi: 10.1093/bioinformatics/btt086. [DOI] [PMC free article] [PubMed] [Google Scholar]

34. Nilsson RH, Larsson K-H, Taylor AFS, Bengtsson-Palme J, Jeppesen TS, Schigel D, Kennedy P, Picard K, Glöckner FO, Tedersoo L, Saar I, Kõljalg U, Abarenkov K. 2019. The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Res 47:D259–D264. doi: 10.1093/nar/gky1022. [DOI] [PMC free article] [PubMed] [Google Scholar]

35. Samson RA, Houbraken J, Thrane U, Frisvad J, Andersen B. 2019. Food and indoor fungi, 2nd ed. Westerdijk Fungal Diversity Institute, Utrecht, The Netherlands. [Google Scholar]

36. Ray S, Gebre S, Fogle H, Berrios DC, Tran PB, Galazka JM, Costes SV. 2019. GeneLab: omics database for spaceflight experiments. Bioinformatics 35:1753–1759. doi: 10.1093/bioinformatics/bty884. [DOI] [PubMed] [Google Scholar]

Associated Data

This section collects any data citations, data availability statements, or supplementary materials included in this article.

Data Availability Statement

The whole-genome sequences (WGSs) and raw data have been deposited in GenBank under BioProject accession number PRJNA723004. This project has also been deposited in the NASA GeneLab system (36) under project number GLDS-400. The version described in this paper is the first version.